

L Number	Hits	Search Text	DB	Time stamp
1	0	mRNA near5 RT-PCR and circular adj1 cDNA	USPAT; US-PGPUB; DERWENT	2003/02/11 12:38
2	1697	mRNA near5 RT-PCR	USPAT; US-PGPUB; DERWENT	2003/02/11 12:38
3	0	(mRNA near5 RT-PCR) and cicular	USPAT; US-PGPUB; DERWENT	2003/02/11 12:38
4	405	(mRNA near5 RT-PCR) and circular	USPAT; US-PGPUB; DERWENT	2003/02/11 12:38
5	332	((mRNA near5 RT-PCR) and circular) and ligat\$	USPAT; US-PGPUB; DERWENT	2003/02/11 12:39
6	62	((mRNA near5 RT-PCR) and circular) and ligat\$) and primer adj1 extension	USPAT; US-PGPUB; DERWENT	2003/02/11 12:44
7	205	(mRNA near5 RT-PCR) and RNase adj1 H	USPAT; US-PGPUB; DERWENT	2003/02/11 12:50
8	21	circular adj1 cDNA	USPAT; US-PGPUB; DERWENT	2003/02/11 13:31
9	409	Reverse adj1 transcriptase near5 RNase adj1 H	USPAT; US-PGPUB; DERWENT	2003/02/11 13:32
10	5	(Reverse adj1 transcriptase near5 RNase adj1 H) and circular adj1 cDNA	USPAT; US-PGPUB; DERWENT	2003/02/11 13:32



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☐ 1: Anal Biochem 1995 May 20;227(2):255-73

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ELSEVIER SCIENCE
FULL-TEXT ARTICLE

Revolutions in rapid amplification of cDNA ends: new strategies for polymerase chain reaction cloning of full-length cDNA ends.

Schaefer BC.

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Division of Tumor Virology, Dana-Farber Cancer Institute, Boston, Massachusetts 02115, USA.

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Rapid amplification of cDNA ends (RACE) is a polymerase chain reaction (PCR)-based technique which was developed to facilitate the cloning of full-length cDNA 5'- and 3'-ends after a partial cDNA sequence has been obtained by other methods. While RACE can yield complete sequences of cDNA ends in only a few days, the RACE procedure frequently results in the exclusive amplification of truncated cDNA ends, undermining efforts to generate full-length clones. Many investigators have suggested modifications to the RACE protocol to improve the effectiveness of the technique. Based on first-hand experience with RACE, a critical review of numerous published variations of the key steps in the RACE method is presented. Also included is a detailed, effective protocol based on RNA ligase-mediated RACE/reverse ligation-mediated PCR, as well as a demonstration of its utility.

Publication Types:

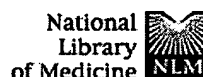
- Review
- Review, Tutorial

PMID: 7573945 [PubMed - indexed for MEDLINE]

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☐ 1: Curr Issues Mol Biol 1999;1(1-2):13-20

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Synthesis of infectious viroids and other circular RNAs.

Rezaian MA.

PubMed
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CSIRO Plant Industry Horticulture Unit, Adelaide Laboratory, PO Box 350, Glen Osmond, SA 5064, Australia.

Related
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Viroids are small autonomously replicating RNAs that share structural features with other subviral circular single-stranded RNAs of plants. Viroids and other circular single-stranded RNAs can be synthesised in vitro by a PCR-based procedure using a simple set of reactions. Two end-to-end primers are selected from a desired region of the viroid, one for the synthesis of the first strand cDNA and another for the production of the second strand DNA. The second primer contains an 18 nucleotide T7 promoter at its 5' end, and is selected such that the G nucleotide at the transcription start site represents a G in the viroid. Linked reverse transcription-PCR results in linear double-stranded DNA consisting of the viroid sequence and the T7 promoter. Run-off transcription of the PCR product allows the synthesis of exact-length linear viroid RNA which can be circularised by T4 RNA ligase following an enzymic modification of the 5' triphosphate to a monophosphate. This procedure results in authentic viroid molecules and obviates the need for construction and cloning of DNA in the form of tandem repeats for infectivity tests. It also allows PCR-based manipulation of circular RNAs, thus greatly simplifying structure-function analyses of viroid molecules.

PMID: 11475697 [PubMed - indexed for MEDLINE]

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File View Edit Tools Window Help

00:09: L18: (933) 117 and unknown

Active

- L1: (25516) mRNA
- L2: (351190) linear and single strand
- L3: (687817) circular\$
- L4: (32370) ligase or ligat\$
- L5: (27159) PCR
- L6: (17910) 11 and 12
- L7: (4858) 16 and 13
- L8: (4164) 17 and 14
- L9: (3157) 18 and 15
- L10: (0) 19 and touch-down
- L11: (1181588) touch down PCR
- L12: (10) 19 and touchdown
- L13: (4287224) 19 and reverse transcrip
- L14: (3145) 19 and 113
- L15: (1391) 114 and degenerate
- L16: (1366) 115 and cDNA
- L17: (1252) 116 and ends

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